



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 140902

TO: Karen A Lacourciere
Location: REM-2D15/2C18
Art Unit: 1635
Wednesday, December 29, 2004

Case Serial Number: 08945805

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

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STIC-Biotech/ChemLib

140902

From: Lacourciere, Karen
Sent: Monday, December 20, 2004 3:00 PM
To: STIC-Biotech/ChemLib
Subject: RE: Sequence search request 90/006175

Please search this using the CRF from 08945805

Thank-you!

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Monday, December 20, 2004 2:52 PM
To: Lacourciere, Karen
Subject: RE: Sequence search request 90/006175

There is no valid CRF for this serial number, please provide us with another valid serial number. Thank you. Linda

-----Original Message-----

From: Lacourciere, Karen
Sent: Monday, December 20, 2004 2:33 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search request 90/006175

Please search SEQ ID NO:1 for 90/006,175 in both the commercial databases and in the pending files (interference)
Thank-you

Karen A. Lacourciere Ph.D.
Remsen 2D15 GAU 1635
(571) 272-0759

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search
NA Sequence: # _____
AA Sequence :# _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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SEQUENCE LISTING WARNING:

The sequence serial number you submitted was not listed in the CRF file. The attached search may not contain the exact sequence(s) listed under your serial number. The sequence listing used was in the CRF for an earlier serial number. The file wrapper of your case indicated it as a CIP, Divisional, Parent, Grandparent, Grandchild(ren) or Continuation of the earlier serial number.

Please remember that it is the examiner's responsibility to ensure that a case is in compliance with the sequence rules before allowing it.

*CRF from 08-945805 (US 626203
used for this search)*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 1772 Seconds
(without alignments)
533.744 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgagggttcctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	6	BD272318
2	20	100.0	20	6	AX937169
3	20	100.0	20	6	BD166242
4	20	100.0	20	6	BD173898
5	20	100.0	36	6	AR211932
6	20	100.0	36	6	AR491437
7	20	100.0	46	6	AR211931
8	20	100.0	46	6	AR491436
9	20	100.0	130	6	AX824437
10	20	100.0	397	11	G73338
11	20	100.0	411	11	G73796
12	20	100.0	604	11	G73795
13	20	100.0	992	10	MMVCAM1B1
14	20	100.0	1032	6	AR174653
15	20	100.0	1032	6	BD140422
16	20	100.0	2321	10	MUSVCAM01
17	20	100.0	2355	9	S50587
18	20	100.0	2396	9	MMVCAMA
19	20	100.0	2458	10	MMU42327

20	20	100.0	2501	6	CQ778548	CQ778548	Sequence
21	20	100.0	3418	10	BC029823	BC029823	Mus muscu
22	20	100.0	3691	6	AX188354	AX188354	Sequence
23	20	100.0	5607	9	HUMVCAM1A	M73255	Human vascu
24	20	100.0	22868	9	AF536818	AF536818	Homo sapi
25	20	100.0	152858	9	AC093428	AC093428	Homo sapi
26	20	100.0	194252	10	AC108909	AC108909	Mus muscu
c 27	20	100.0	228371	2	AC122888	AC122888	Mus muscu
c 28	20	100.0	268180	2	AC113762	AC113762	Rattus no
c 29	20	100.0	287919	2	AC109094	AC109094	Rattus no
c 30	18.4	92.0	110000	1	AE017180_15	Continuation (16 o	
31	18	90.0	19	6	AR211934	AR211934	Sequence
32	18	90.0	19	6	AR491439	AR491439	Sequence
33	18	90.0	160765	2	AC136005	AC136005	Homo sapi
34	18	90.0	161027	9	AC136006	AC136006	Homo sapi
35	18	90.0	169073	8	AC132491	AC132491	Oryza sat
c 36	18	90.0	179599	2	AC112930	AC112930	Mus muscu
37	18	90.0	213073	9	AC092653	AC092653	Homo sapi
38	17.4	87.0	63	6	AX824455	AX824455	Sequence
c 39	17.4	87.0	63	6	AX824456	AX824456	Sequence
40	17.4	87.0	1360	14	AY486462	AY486462	Hyposter
c 41	17.4	87.0	90354	9	AP001124	AP001124	Homo sapi
42	17.4	87.0	166860	10	AC115924	AC115924	Mus muscu
c 43	17.4	87.0	179080	2	AC092514	AC092514	Papio anu
44	17.4	87.0	203822	2	AC146825	AC146825	Otolemur
45	17.4	87.0	219796	2	AC146734	AC146734	Otolemur

ALIGNMENTS

RESULT 1
BD272318

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BD272318 20 bp DNA linear PAT 17-JUL-2003
Method for determining whether a certain compound is able to
inhibit the interaction of peptide with receptor of advanced
glycation end product (RAGE).

BD272318

BD272318.1 GI:33082086

JP 2002526758-A/1.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Schmidt,A.M. and Stern,D.

Method for determining whether a certain compound is able to

inhibit the interaction of peptide with receptor of advanced

glycation end product (RAGE)

Patent: JP 2002526758-A 1 20-AUG-2002;

THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

OS Homo sapiens (human)

PN JP 2002526758-A/1

PD 20-AUG-2002

PF 05-OCT-1999 JP 2000574569

PR 05-OCT-1998 US 09/166649

PI ANN MARIE SCHMIDT,DAVID STERN

PC GOIN33/50,A61K9/12,A61K9/127,A61K9/50,A61K31/472,A61K45/00, PC

A61P3/00,

PC

A61P3/04,A61P3/10,A61P3/12,A61P29/00,A61P37/06,C12Q1/02,C12Q1/ PC

68,

GOIN33/15//C12N5/10,C12N5/00

CC Primer Against Human NF-kB

CC PCR Primer Against Human NF-kB

CC Key Location/Qualifiers

FT source 1..20

FT Location/Qualifiers

1..20

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

Wed Dec 29 09:34:01 2004

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ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
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DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 2
AX937169 AX937169 20 bp DNA linear PAT 06-JAN-2004
LOCUS Sequence 9 from Patent WO03091432.
ACCESSION AX937169
VERSION AX937169.1 GI:40713277
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Lee, I.K. and Morishita, R.
TITLE Circular dumbbell decoy oligodeoxynucleotides (cdodn) containing
          dna bindings sites of transcription factors
JOURNAL Patent: WO 03091432-A 9 06-NOV-2003;
          Anges MG, Inc. (JP) ; Lee, In-Kyu (KR)
FEATURES
source 1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Description of Artificial Sequence: NF-7B decoy"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
    |||||
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 3
BD166242 BD166242 20 bp DNA linear PAT 17-JAN-2003
LOCUS Pharmacetical composition containing decoy and utilization
DEFINITION thereof.
ACCESSION BD166242
VERSION BD166242.1 GI:27872054
KEYWORDS JP 2002193813-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
AUTHORS Morishita, R., Aoki, M., Ogiwara, T. and Kawasaki, T.
TITLE Pharmacetical composition containing decoy and utilization thereof
JOURNAL Patent: JP 2002193813-A 1 10-JUL-2002;
          MEDGENE BIOSCIENCE INC
COMMENT OS Artificial Sequence
        PN JP 2002193813-A/1
        PD 10-JUL-2002
        PF 27-DEC-2000 JP 2000399613
        PI RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIO OGIWARA, TOMIO KAWASAKI
        PC A61K31/7088, A61K47/46, A61P9/00, A61P9/10, A61P11/06, A61P13/12,
        PC A61P17/00,
        PC A61P29/00, A61P35/00, C12N15/09, C12N15/00
        CC Description of Artificial Sequence: NF-kappaB decoy FH Key
        Location/Qualifiers
        FT source 1..20
        FT /organism="Artificial Sequence".

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
    |||||
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 4
BD173898 BD173898 20 bp DNA linear PAT 18-FEB-2003
LOCUS Pharmacetical compositions containing decoy and method of using
DEFINITION the same.
ACCESSION BD173898
VERSION BD173898.1 GI:28415231
KEYWORDS WO 02066070-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Morishita, R., Aoki, M., Ogiwara, T., Kaneda, Y. and Nakamura, H.
TITLE Pharmacetical compositions containing decoy and method of using
          the same
JOURNAL Patent: WO 02066070-A 1 29-AUG-2002;
          ANGES MG INC, RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIO OGIWARA,
          YASUFUMI KANEDA, HIROSHIGE NAKAMURA
COMMENT OS Artificial Sequence
        PN WO 02066070-A/1
        PD 29-AUG-2002
        PF 06-FEB-2002 WO 2002JP000990
        PR 20-FEB-2001 JP 01P 044350
        PI RYUICHI MORISHITA, MOTOKUNI AOKI, TOSHIO OGIWARA, YASUFUMI
          KANEDA,
        PI HIROSHIGE NAKAMURA
        PC A61K48/00, A61K31/711, A61K9/06, A61K47/06, A61K47/10, A61P17/00,
        PC A61P17/04
        CC Description of Artificial Sequence: NF-kappaB decoy FH Key
        Location/Qualifiers
        FT source 1..20
        FT /organism="Artificial Sequence".

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
    |||||
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 5
AR211932 AR211932 36 bp DNA linear PAT 20-JUN-2002
LOCUS Sequence 2 from patent US 6399376.
DEFINITION
ACCESSION AR211932
VERSION AR211932.1 GI:21515384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
          Unclassified.
```


REFERENCE 1 (bases 1 to 36)
AUTHORS Medford,R.M. and Bennett,C.Frank.
TITLE Modulation of vascular cell adhesive molecule expression through
oligonucleotide interactions
JOURNAL Patent: US 6399376-A 2 04-JUN-2002;
FEATURES Location/Qualifiers
source
1..36
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 16 CCTGAAGGGATTCCCTCC 35

RESULT 6
AR491437
LOCUS AR491437 36 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 2 from patent US 6713621.
ACCESSION AR491437
VERSION AR491437.1 GI:47259436
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 36)
AUTHORS Medford,R.M. and Bennett,C.F.
TITLE Chimeric oligonucleotides for modulating gene expression
JOURNAL Patent: US 6713621-A 2 30-MAR-2004;
FEATURES Location/Qualifiers
source
1..36
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 16 CCTGAAGGGATTCCCTCC 35

RESULT 7
AR211931
LOCUS AR211931 46 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from patent US 6399376.
ACCESSION AR211931
VERSION AR211931.1 GI:21515383
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Medford,R.M. and Bennett,C.Frank.
TITLE Modulation of vascular cell adhesive molecule expression through
oligonucleotide interactions
JOURNAL Patent: US 6399376-A 1 04-JUN-2002;
FEATURES Location/Qualifiers
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1..46
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 21 CCTGAAGGGATTCCCTCC 40

RESULT 8
AR491436
LOCUS AR491436 46 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 1 from patent US 6713621.
ACCESSION AR491436
VERSION AR491436.1 GI:47259435
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Medford,R.M. and Bennett,C.F.
TITLE Chimeric oligonucleotides for modulating gene expression
JOURNAL Patent: US 6713621-A 1 30-MAR-2004;
FEATURES Location/Qualifiers
source
1..46
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/mol_type="genomic DNA"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 21 CCTGAAGGGATTCCCTCC 40

RESULT 9
AX824437
LOCUS AX824437 130 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 16 from Patent WO03071281.
ACCESSION AX824437
VERSION AX824437.1 GI:39750436
KEYWORDS
SOURCE Synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boersma,C.J. and van Gool,A.J.
TITLE Estrogen receptor interaction with a transcription factor
JOURNAL Patent: WO 03071281-A 16 28-AUG-2003;
Akzo Nobel N.V. (NL)
FEATURES Location/Qualifiers
source
1..130
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="vCAM-1, sequence of cloned part on page 32 lines
4-7"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 130;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTGAAGGGATTCCCTCC 20
Db 34 CCTGAAGGGATTCCCTCC 53

RESULT 10
G73338
LOCUS G73338 397 bp DNA linear STS 28-DEC-2002
DEFINITION SGV-R233 Genomic DNA from human peripheral blood leukocytes Homo
sapiens STS genomic 5' and 3', sequence tagged site.

Wed Dec 29 09:34:01 2004

ACCESSION G73338
 VERSION G73338.1 GI:27413062
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 397)
 REFERENCE Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I.,
 Serjeant,G.R., Rodgers,G.P. and Chanock,S.J.
 TITLE Variants in the VCAM1 gene and risk for symptomatic stroke in
 sickle cell disease
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for
 Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle,
 Gaithersburg, MD 20877, USA
 Email: sc83a@nih.gov
 Primer A: AGTGAAGTGGCTGGGTG
 Primer B: TCACCTACTATCGCAAACTGACTG
 STS size: 397
 PCR Profile:
 Preincubation: 95 degrees C for 600 seconds
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 63 degrees C for 30 seconds
 Extension: 72 degrees C for 40 seconds
 Final Extension: 72 degrees C for 600 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 AmpliTaqGold Polymerase: 0.025 units/ul
 Total Vol: 20 ul
 Buffer:
 MgCl2 1.8 mM
 Applied Biosystems 10X PCR Buffer II 1X volume
 Exon 1 ; The 5' end of PCR primers were tagged with a universal
 sequencing primer; either M13P (TGTAAAACGACGGCCAGT) for forward
 primers or M13R (CAGGAACAGCTATGACC) for reverse primers.
 FEATURES
 source
 1..397
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Genomic DNA from human peripheral blood
 leukocytes"
 /note="Human genomic DNA prepared from either fresh or
 immortalized peripheral blood leukocytes"
 1..397
 /gene="VCAM1"
 /note="Vascular cell adhesion molecule 1"
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 1..19
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 primer_bind
 primer_bind
 complement(374..397)
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 Best Local Similarity 100.0%; Pred. No. 6.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAAGGATTCCTCC 20
 |||||||
 Db 59 CCTTGAAGGATTCCTCC 78

RESULT 11
 G73796
 LOCUS
 DEFINITION SGV-R137 Genomic DNA from human peripheral blood leukocytes Homo
 sapiens STS genomic 5' and 3', sequence tagged site.
 G73796
 ACCESSION G73796.1 GI:27413076
 VERSIONS
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 411)
 REFERENCE Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I.,
 Serjeant,G.R., Rodgers,G.P. and Chanock,S.J.
 TITLE Variants in the VCAM1 gene and risk for symptomatic stroke in
 sickle cell disease
 JOURNAL Unpublished (2001)
 COMMENT Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for
 Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle,
 Gaithersburg, MD 20877, USA
 Email: sc83a@nih.gov
 Primer A: TTTTTCCTCTCCACACCC
 Primer B: AACCTTATTTGTGCCACCTG
 STS size: 411
 PCR Profile:
 Preincubation: 95 degrees C for 600 seconds
 Denaturation: 94 degrees C for 30 seconds
 Annealing: 63 degrees C for 30 seconds
 Extension: 72 degrees C for 40 seconds
 Final Extension: 72 degrees C for 600 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 AmpliTaqGold Polymerase: 0.025 units/ul
 Total Vol: 20 ul
 Buffer:
 MgCl2 1.8 mM
 Applied Biosystems 10X PCR Buffer II 1X volume
 5' upstream region.
 FEATURES
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 1..411
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Genomic DNA from human peripheral blood
 leukocytes"
 /note="Human genomic DNA prepared from either fresh or
 immortalized peripheral blood leukocytes"
 1..411
 /gene="VCAM1"
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 1..411
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 complement(389..411)
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 Best Local Similarity 100.0%; Pred. No. 6.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 262 CCTTGAAGGGATTTCCTCC 281

RESULT 12

G73795 604 bp DNA linear STS 28-DEC-2002
 LOCUS SGV-R136 Genomic DNA from human peripheral blood leukocytes Homo
 DEFINITION sapiens STS genomic 5' and 3', sequence tagged site.
 G73795
 VERSION G73795.1 GI:27413075
 KEYWORDS STS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 604)
 REFERENCE Taylor,J.G., Tang,D., Savage,S., Leitman,S.F., Heller,S.I.,
 AUTHORS Serjeant,G.R., Rodgers,G.P. and Chanock,S.J.
 TITLE Variants in the VCAM1 gene and risk for symptomatic stroke in
 sickle cell disease
 JOURNAL Unpublished (2001)
 COMMENT

Contact: Stephen J. Chanock
 Section of Genomic Variation, Pediatric Oncology Branch, Center for
 Cancer Research, National Cancer Institute
 National Institutes of Health
 NCI Advanced Technology Center, 8717 Grovemont Circle,
 Gaithersburg, MD 20877, USA
 Email: sc83@nih.gov
 Primer A: GAAGTTATGGTGTCCCTTTT
 Primer B: AACCTTATTGTGCTCCAC
 STS size: 604

PCR Profile:

Denaturation: 95 degrees C for 600 seconds
 Annealing: 94 degrees C for 30 seconds
 Extension: 55 degrees C for 30 seconds
 Final Extension: 72 degrees C for 40 seconds
 PCR Cycles: 40
 Thermal cycler: MJ Research model PTC-225
 Protocol:
 Template: 10-50 ng
 Primer: each 0.5 uM
 dNTPs: each 200 uM
 AmpliTaqGold Polymerase: 0.025 units/ul
 Total Vol: 20 ul

Buffer:

MgCl2 1.8 mM
 Applied Biosystems 10X PCR Buffer II 1X volume

5' upstream region.

FEATURES
 source
 Location/Qualifiers
 1..604
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Genomic DNA from human peripheral blood
 leukocytes"
 /note="Human genomic DNA prepared from either fresh or
 immortalized peripheral blood leukocytes"
 gene 1..604
 /gene="VCAM1"
 /note="vascular cell adhesion molecule 1"
 STS 1..604
 /gene="VCAM1"
 primer_bind 1..22
 /gene="VCAM1"
 primer_bind complement(585..604)

ORIGIN

Query Match 100.0%; Score 20; DB 11; Length 604;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 455 CCTTGAAGGGATTTCCTCC 474
 RESULT 13
 MMVCAM1B1
 LOCUS Mus musculus NIH Swiss vascular cell adhesion molecule-1 (VCAM-1)
 DEFINITION gene, exon 1, partial cds.
 ACCESSION U12878
 VERSION U12878.1 GI:1041794
 KEYWORDS 1 of 6
 SEGMENT
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 796; 808 to 824)
 REFERENCE Kumar,A.G., Dai,Y.X., Kozak,C.A., Mims,M.P., Gotto,A.M. and
 AUTHORS Ballantyne,C.M.
 TITLE Murine VCAM-1: Molecular cloning, Mapping, and Analysis of a
 Truncated Form
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 992)
 AUTHORS Kumar,A.G.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-1994) Ajith G. Kumar, Department of Medicine,
 Baylor College of Medicine, 6535 Fannin Street, Houston, TX 77030,
 USA
 COMMENT On Oct 28, 1995 this sequence version replaced gi:531856.
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 Location/Qualifiers
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 Jolla, CA"
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 CDS 751..>814
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 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCTTGAAGGGATTTCCTCC 20
 Db 592 CCTTGAAGGGATTTCCTCC 611
 RESULT 14

Wed Dec 29 09:34:01 2004

AR174653
LOCUS AR174653 1032 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6307025.
ACCESSION AR174653
VERSION AR174653.1 GI:17914973
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Hession,C.A., Lobb,R.R., Goelz,S.E., Osborn,L., Benjamin,C.D. and Rosa,M.D.
TITLE VCAM fusion proteins and DNA coding therefor
JOURNAL Patent: US 6307025-A 8 23-OCT-2001;
FEATURES
Location/Qualifiers
1..1032
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ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 1032;
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Matches 20; Conservative 0; Mismatches 0;
QY 1 CCTTGAAGGGATTCCCTCC 20
|||||
Db 221 CCTTGAAGGGATTCCCTCC 240

RESULT 15

BD140422 1032 bp DNA linear PAT 18-SEP-2002
LOCUS BD140422
DEFINITION Endothelial-leukocyte adhesion molecule (ELAM) and molecule participating in leukocyte adhesion (MILA).
ACCESSION BD140422
VERSION BD140422.1 GI:23235367
KEYWORDS JP 2002065285-A/6.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Hession,C.R., Lobb,R.R., Goelz,S.E., Osborne,L., Benjamin,C.D. and Rosa,M.D.
TITLE Endothelial-leukocyte adhesion molecule (ELAM) and molecule participating in leukocyte adhesion (MILA)
JOURNAL Patent: JP 2002065285-A 6 05-MAR-2002;
BIOGEN INC

COMMENT

OS Homo sapiens (human)
PN JP 2002065285-A/6
PD 05-MAR-2002
PF 18-JUN-2001 JP 2001184133 359516 PR
PR 28-APR-1989 US 452675
18-DEC-1989 US
PI CATHERINE R HESSON,ROY R LOBB,SUSAN E GOELZ,LAURELY OSBORNE,
PI CHRISTOPHER D BENJAMIN,MARGARET D ROSA
PC C12N15/09,A61K35/16,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
A61P17/00,
PC A61P35/00,C07K14/47,C07K16/18,C07K16/42,C12N1/15,C12N1/19, PC
C12N1/21,
PC
C12N5/10,C12N5/10,C12N5/10,C12N15/02,C12P21/02,C12P21/08,C12Q1/ PC
02,
PC G01N33/15,G01N33/50,G01N33/53,G01N33/53,G01N33/566,G01N33/577,
PC C12N15/00,
PC C12N5/00,C12N15/00,C12N5/00,A61K37/02,C12N5/00 CC
Endothelial-leukocyte adhesion molecule (ELAM) and molecule CC
participating
CC in leukocyte adhesion (MILA)
FH key Location/Qualifiers
FT source 1..1032
/organism='Homo sapiens (human)'.
FT Location/Qualifiers

FEATURES

source
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|||||
Db 221 CCTTGAAGGGATTCCCTCC 240
Search completed: December 28, 2004, 10:45:37
Job time : 1778 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 399 Seconds
(without alignments)
263.129 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 cctgaagggttcctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	2	Aat69675
2	20	100.0	20	3	Aa14365
3	20	100.0	20	4	Aa43069
4	20	100.0	20	6	Abv72301
5	20	100.0	20	6	Ab54472
6	20	100.0	20	9	Acc79778
7	20	100.0	20	10	Add69731
8	20	100.0	20	10	Adf53868
9	20	100.0	20	10	Adg43792
10	20	100.0	20	12	Adf69631
11	20	100.0	20	12	Adm91765
12	20	100.0	20	12	Adp83986
13	20	100.0	36	2	Aa90101
14	20	100.0	47	2	Aa90100
15	20	100.0	130	10	Acf79417
16	20	100.0	1024	10	Abz83493
17	20	100.0	1032	2	Aa906690
18	20	100.0	1032	6	Aa17081
19	20	100.0	1032	10	Adh73058
20	20	100.0	2396	3	Aa34966
21	20	100.0	2396	3	Aaf21088

ALIGNMENTS

RESULT 1

AAT69675

ID AAT69675 standard; DNA; 20 BP.

XX AC AAT69675;

XX DT 04-AUG-1997 (first entry)

XX DE Transcription factor NF-kappa-B DNA binding site antagonist.

XX KW Decoy; antagonist; NF-kappa-B; NF-kB; transcription; regulation;

XX KW prevention; treatment; disease; ischaemia; inflammation;

XX KW autoimmune; cancer; metastasis; cachexia; organ; transplantation;

XX KW surgery; ds.

XX OS Synthetic.

XX PN WO9635430-A1.

XX PD 14-NOV-1996.

XX PF 10-MAY-1996; 96WO-JP001234.

XX PR 12-MAY-1995; 95JP-00114990.

XX PR 02-NOV-1995; 95JP-00285504.

XX PA (FUJI) FUJISAWA PHARM CO LTD.

XX PI Morishita R, Ogiwara T, Sugimoto T, Maeda K, Kawamura I, Chiba T;

XX DR WPI; 1996-518400/51.

XX XX

XX PT Anti:sense NF-kB agent - for treatment of ischaemia, inflammatory disease

XX PT auto:immune disease, etc.

XX XX

XX PS Claim 7; Page 9; 18pp; Japanese.

XX XX

XX CC The present sequence is a decoy, which specifically antagonises the

XX CC nucleic acid site to which a NF-kappa-B transcription regulator binds. It

XX CC can be used to prevent or treat diseases caused by NF-kappa-B, e.g.

XX CC ischaemia, inflammatory and autoimmune disease, cancer metastasis and

XX CC cachexia, especially following organ transplant or surgery

XX XX

XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

22	20	100.0	2396	10	ABZ96782	Abz96782 Human nuc
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25	20	100.0	3691	4	AAH72772	Aah72772 Human cer
26	20	100.0	4616	3	AAA34968	Aaa34968 Human ade
27	20	100.0	4616	3	AAF21090	Aaf21090 Human low
28	20	100.0	4616	10	ABZ96784	Abz96784 Human nuc
29	20	100.0	4616	11	ABD20633	Abd20633 Human pul
30	18	90.0	19	2	AAQ90103	Aa90103 VCAM-1 ex
31	17.4	87.0	63	10	ACF79431	Acf79431 VCAM 3 PC
32	17.4	87.0	63	10	ACF79432	Acf79432 VCAM 3 PC
33	17	85.0	708	6	ABZ42918	Abz42918 Human gpc
34	16.8	84.0	37	11	ADL76518	Adl76518 Human ptg
35	16.8	84.0	40	12	ADG13972	Adg13972 Human egf
36	16.8	84.0	40	12	ADG13997	Adg13997 Human egf
37	16.8	84.0	40	12	ADG14001	Adg14001 Human egf
38	16.8	84.0	40	12	ADG14005	Adg14005 Human egf
39	16.8	84.0	40	12	ADG13983	Adg13983 Human egf
40	16.8	84.0	40	12	ADG14002	Adg14002 Human egf
41	16.8	84.0	40	12	ADG13980	Adg13980 Human egf
42	16.8	84.0	40	12	ADG13979	Adg13979 Human egf
43	16.8	84.0	40	12	ADG13981	Adg13981 Human egf
44	16.8	84.0	40	12	ADG13989	Adg13989 Human egf
45	16.8	84.0	40	12	ADG13976	Adg13976 Human egf

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XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
SQ Query Match 100.0%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 2
AA14365
ID AAA14365 standard; DNA; 20 BP.
XX
AC AAA14365;
XX
DT 15-AUG-2000 (first entry)
XX
DE Human NF-kappa-B binding site EMSA probe.
XX
KW NK-kappa-B binding site; nuclear factor-kappa-B; EMSA;
KW electrophoretic mobility shift assay; advanced glycation end-product;
KW AGE; receptor for AGE; RAGE; interaction inhibitor; kidney failure;
KW diabetes; systemic lupus erythematosus; inflammatory lupus nephritis;
KW obesity; amyloidosis; inflammation; ageing; ds.
XX
OS Homo sapiens.
XX
PN WO200020458-A1.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-US02245.
XX
PR 05-OCT-1998; 98US-00166649.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Schmidt AM, Stern D;
XX
DR WPI; 2000-303750/26.
XX
PT Determining inhibitors of interaction between an advanced glycation
PT endproduct and its receptor, useful to develop therapeutics for various
PT associated conditions including diabetes and inflammatory lupus
PT nephritis.
XX
PS Example 1; Page 30; 66pp; English.
XX
CC The invention relates to a novel method for determining whether a
CC compound can inhibit interaction of an advanced glycation end-product
CC (AGE) or fragment thereof with the receptor for AGEs (RAGE). The method
CC comprises admixing the AGE (which has its amino groups inactivated by
CC chemical derivatization), RAGE, and the compound; determining the amount
CC of peptide bound to RAGE, and comparing this amount to the amount of
CC binding in the absence of the compound. A decrease in AGE/RAGE binding in
CC the presence of the compound indicates that the compound is an inhibitor.
CC Exemplary inhibitory compounds identified via the method are quinine,
CC quinine, or derivatives with the same overall charge as these
CC compounds. AGEs are a class of compounds with heterogeneous structures
CC that result from the process of glycooxidation. The accumulation of AGEs
CC has been linked to a range of complications that occur in disorders such
CC as ageing, diabetes, renal failure and inflammation. Interaction of an
CC AGE with RAGE triggers multiple mechanisms, including the activation of
CC NF-kappa-B (nuclear factor kappa-B) which result in cellular perturbation
CC and dysfunction. Compounds which inhibit the interaction between AGEs and
CC RAGE may be used to treat kidney failure, diabetes, systemic lupus
CC erythematosus, inflammatory lupus nephritis, obesity, amyloidosis or
CC inflammation. Administration of such compounds may also be of benefit to
CC elderly individuals, particularly humans, other primates, mice, rats or
CC dogs. The present sequence represents an NF-kappa-B binding site probe
CC used in electrophoretic mobility shift assays (EMSA) of nuclear extracts
CC of human umbilical vein endothelial cells (HUEVCs) previously treated
```

```
ABV72301
ID ABV72301 standard; DNA; 20 BP.
XX
XX AC ABV72301;
XX
XX DT 16-DEC-2002 (first entry)
XX
XX DE Nucleotide sequence of nuclear factor (NF)-kappaB decoy.
XX
XX KW Nuclear factor-kappaB; NF-kappa B; decoy; ets; disease; ds.
XX
XX OS Synthetic.
XX
XX PN JP2002193813-A.
XX
XX PD 10-JUL-2002.
XX
XX PF 27-DEC-2000; 2000JP-00399613.
XX
XX PR 27-DEC-2000; 2000JP-00399613.
XX
XX PA (ANJE-) ANJESU MG KK.
XX
XX DR WPI; 2002-660723/71.
XX
XX A pharmacological composition containing a decoy compound for treating
PT diseases caused by the expression of a gene controlled by NF-kappaB or
PT ets.
XX
XX PS Example 1; Page 9; 18pp; Japanese.
XX
XX CC The present sequence represents a synthetic nuclear factor (NF)-kappa B
CC decoy. The specification describes a pharmacological composition for
CC treating and preventing diseases caused by the expression of a gene
CC controlled by NF-kappaB or ets. The composition comprises at least one
CC decoy compound and a pharmacologically allowable carrier. The composition
CC is used for treating diseases caused by the expression of a gene
CC controlled by NF-kappaB or ets
XX
XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Qy 1 CCTTGAAGGGATTCCCTCC 20
XX |||||||
XX Db 1 CCTTGAAGGGATTCCCTCC 20
XX |||||||
XX
XX RESULT 5
XX ABS54472
XX ID ABS54472 standard; DNA; 20 BP.
XX
XX AC ABS54472;
XX
XX DT 11-DEC-2002 (first entry)
XX
XX DE Nuclear factor (NF)-kappa B decoy oligonucleotide.
XX
XX KW NF-kappa B; ss; drug composition; skin disease; decoy;
XX nuclear factor-kappa B; signal transducer and activator of transcription;
XX STAT-1; STAT-6; GATA-3; activator protein-1; AP-1; Ets;
XX atopic dermatitis; psoriasis vulgaris; contact dermatitis; keloid;
XX bedsores; ulcerative colitis; Crohn's disease.
XX
XX OS Synthetic.
XX
XX PN WO200266070-A1.
XX
XX PD 29-AUG-2002.
XX
XX PF 06-FEB-2002; 2002WO-JP000990.
XX
XX Query Match 100.0%; Score 20; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTTGAAGGGATTCCCTCC 20
XX |||||||
XX Db 1 CCTTGAAGGGATTCCCTCC 20
XX |||||||
XX
XX RESULT 6
XX ACC79778
XX ID ACC79778 standard; DNA; 20 BP.
XX
XX AC ACC79778;
XX
XX DT 29-AUG-2003 (first entry)
XX
XX DE Nuclear factor-kappa B (NF-kappa-B) decoy oligonucleotide SEQ ID NO:1.
XX
XX KW Pharmaceutical composition; organ transplantation rejection inhibition;
XX immunosuppressive; regeneration; transplantation medicine;
XX kidney transplant; nuclear factor-kappa B; NF-kappa-B; ss.
XX
XX OS Synthetic.
XX
XX PN WO2003043663-A1.
XX
XX PD 30-MAY-2003.
XX
XX PF 20-NOV-2002; 2002WO-JP012142.
XX
XX PR 22-NOV-2001; 2001JP-00358587.
XX
XX PA (ANGE-) ANGES MG INC.
XX
XX PI Morishita R, Tomita N, Ogiwara T, Higashi N;
XX WPI; 2003-541462/51.
XX
XX Pharmaceutical compositions, useful for the suppression of rejection in
PT organ transplantation e.g. kidney transplants, comprises a nuclear
PT transcription factor (NF-kappa-B) decoy compound and optionally an
PT ultrasonic test contrast medium.
XX
XX PS Example; Page 10; 42pp; Japanese.
```

```
XX
XX 20-FEB-2001; 2001JP-00044350.
XX (ANGE-) ANGES MG INC.
XX
XX PI Morishita R, Aoki M, Ogiwara T, Kaneda Y, Nakamura H;
XX
XX DR WPI; 2002-732717/79.
XX
XX Compositions for treating diseases, such as, atopic dermatitis, psoriasis
PT vulgaris, contact dermatitis, and ulcerative colitis comprises decoys of
PT e.g. nuclear factor-kappaB, and signal transducer and activator of
PT transcription.
XX
XX Disclosure; Page 8; 41pp; Japanese.
XX
XX The invention discloses drug compositions for treating skin diseases
CC containing a decoy and a pharmaceutically-acceptable carrier. The decoy
CC oligonucleotides affect genes including nuclear factor (NF)-kappa B,
CC signal transducer and activator of transcription (STAT)-1 and 6, GATA-3,
CC activator protein (AP)-1 and Ets. The drug compositions are applicable in
CC treating skin diseases like atopic dermatitis, psoriasis vulgaris,
CC contact dermatitis, keloid, bedsores, ulcerative colitis or Crohn's
CC disease. The sequence presented is the decoy oligonucleotide for NF-kappa
CC B
XX
XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.9;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCTTGAAGGGATTCCCTCC 20
XX |||||||
XX Db 1 CCTTGAAGGGATTCCCTCC 20
XX |||||||
XX
XX RESULT 6
XX ACC79778
XX ID ACC79778 standard; DNA; 20 BP.
XX
XX AC ACC79778;
XX
XX DT 29-AUG-2003 (first entry)
XX
XX DE Nuclear factor-kappa B (NF-kappa-B) decoy oligonucleotide SEQ ID NO:1.
XX
XX KW Pharmaceutical composition; organ transplantation rejection inhibition;
XX immunosuppressive; regeneration; transplantation medicine;
XX kidney transplant; nuclear factor-kappa B; NF-kappa-B; ss.
XX
XX OS Synthetic.
XX
XX PN WO2003043663-A1.
XX
XX PD 30-MAY-2003.
XX
XX PF 20-NOV-2002; 2002WO-JP012142.
XX
XX PR 22-NOV-2001; 2001JP-00358587.
XX
XX PA (ANGE-) ANGES MG INC.
XX
XX PI Morishita R, Tomita N, Ogiwara T, Higashi N;
XX WPI; 2003-541462/51.
XX
XX Pharmaceutical compositions, useful for the suppression of rejection in
PT organ transplantation e.g. kidney transplants, comprises a nuclear
PT transcription factor (NF-kappa-B) decoy compound and optionally an
PT ultrasonic test contrast medium.
XX
XX PS Example; Page 10; 42pp; Japanese.
```

Wed Dec 29 09:34:03 2004

CC and may be useful for the prevention of brain and nerve injury following
 CC disorders associated with cerebral ischaemia, such as sub-cranial
 CC membrane bleeding, hypertensive intracranial bleeding, cerebral
 CC infarction, brain tumour or chronic or acute subdural haematoma. The
 CC current sequence is that of the cerebral ischaemia-related NF-kappaB
 CC decoy DNA of the invention.
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
 QY 1 CCTTGAAGGGATTTCCTCC 20
 |||||
 DB 1 CCTTGAAGGGATTTCCTCC 20
 |||||
 RESULT 8
 ADF53868
 ID ADF53868 standard; DNA; 20 BP.
 XX
 AC ADF53868;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Circular dumbbell oligodeoxynucleotide related oligo, SEQ ID NO 9.
 KW circular dumbbell oligodeoxynucleotide; CDODN; DNA-binding domain;
 KW transcriptional factor; vasotropic; antiinflammatory; gastrointestinal;
 KW dermatological; antiarteriosclerotic; antiatherosclerotic; cytostatic;
 KW antiasthmatic; gene therapy; AP-1 decoy; E2F decoy;
 KW vascular smooth muscle cell proliferation; neointimal hyperplasia;
 KW restenosis; prophylaxis; exonuclease; ss.
 XX
 OS Unidentified.
 XX
 FN WO2003091432-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 26-APR-2002; 2002WO-JP004303.
 XX
 PR 26-APR-2002; 2002WO-JP004303.
 XX
 PA (ANGE-) ANGES MG INC.
 PA (LEEI) LEE I.
 XX
 PI Lee I, Morishita R;
 XX
 WPI; 2003-877331/81.
 XX
 DR New circular dumbbell oligonucleotide comprising two loops and a stem
 PT structure capable of binding the DNA-binding domain of AP-1, E2F or
 PT NFkappaB, useful in treating or preventing vascular smooth muscle cell
 PT proliferation.
 XX
 PS Disclosure; SEQ ID NO 9; 142pp; English.
 XX
 CC The invention relates to a novel circular dumbbell oligodeoxynucleotide
 CC (CDODN) comprising two loop structures and a stem structure, where the
 CC stem structure comprises a nucleotide sequence capable of binding the DNA
 CC -binding domain of a transcriptional factor. The invention further
 CC comprises a method for treating or preventing a disease or disorder
 CC related to a transcriptional factor in a subject; and a pharmaceutical
 CC composition for treating or preventing a disease or disorder related to a
 CC transcriptional factor in a subject comprising a therapeutic amount of a
 CC CDODN described above and a pharmaceutical carrier. The CDODN oligo has
 CC the following activities: vasotropic, antiinflammatory, gastrointestinal,
 CC dermatological, antiarteriosclerotic, antiatherosclerotic, cytostatic, and
 CC antiasthmatic. The CDODN can be used in gene therapy. The CDODN are
 CC useful in the manufacture of a medicament for treating or preventing a
 CC disease or disorder related to a transcriptional factor in a subject. The

XX The present invention describes pharmaceutical compositions (A) for
 CC inhibiting rejection in organ transplantation which contain a nuclear
 CC factor-kappa B (NF-kappa-B) decoy compound. Also described: (1) a method
 CC for inhibiting rejection in organ transplantation by administering any of
 CC the remedies (A) to a donor organ before ultrasonication of the decoy
 CC compound-containing donor organ; (2) a method for improving prognosis of
 CC organ transplantation by administering any of the remedies (A) to a donor
 CC organ before ultrasonication of the decoy compound-containing donor organ
 CC ; and (3) a method for elevating transfection of an oligonucleotide into
 CC a biological tissue by administering such oligonucleotide to a donor
 CC organ before ultrasonication of the oligonucleotide-containing biological
 CC tissue. (A) have immunosuppressive activity, and can be used in NF-kappa-
 CC B inhibitors. The remedies (A) can be used in regeneration and
 CC transplantation medicine. Specifically, they are for inhibiting rejection
 CC in organ transplantation and improving its prognosis, particularly kidney
 CC transplants. The present sequence represents an NF-kappa-B decoy
 CC oligonucleotide, which is used in an example from the present invention
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;
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 DB 1 CCTTGAAGGGATTTCCTCC 20
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 RESULT 7
 ADD69731
 ID ADD69731 standard; DNA; 20 BP.
 XX
 AC ADD69731;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Cerebral ischaemia-related NF-kappaB decoy DNA.
 KW cerebral ischaemia; nuclear factor kappaB; NF-kB decoy; neuroprotective;
 KW neurotropic; cerebroprotective; brain tumour; nerve injury;
 KW sub-cranial membrane bleeding; hypertensive intracranial; infarction;
 KW chronic; acute subdural haematoma; ds.
 XX
 OS Unidentified.
 XX
 FN WO2003082331-A1.
 XX
 PD 09-OCT-2003.
 XX
 PF 29-MAR-2002; 2002WO-JP003239.
 XX
 PR 29-MAR-2002; 2002WO-JP003239.
 XX
 PA (ANGE-) ANGES MG INC.
 PA (SAWA) SAWA Y.
 XX
 PI Sawa Y, Morishita R, Kaneda Y, Matsuda H, Yoshimine T;
 XX
 WPI; 2003-812508/76.
 XX
 DR Transfection of NF-kB decoy oligonucleotide into brain tissue by carotid
 PT injection using a suitable carrier for treatment and prevention of
 PT disorders associated with cerebral ischemia.
 XX
 PS Example 1; SEQ ID NO 1; 79pp; Japanese.
 XX
 CC The invention relates to a novel drug composition for prevention and
 CC treatment of disorders associated with cerebral ischaemia which contains
 CC a nuclear factor kappaB (NF-kB) decoy oligonucleotide together with a
 CC suitable carrier for its transfection. The composition of the invention
 CC demonstrates neuroprotective, neurotropic and cerebroprotective activities

CC CDOON or the composition or the AP-1 decoy or E2F decoy is useful in
CC treating or preventing a disease or disorder related to a transcriptional
CC factor, e.g. vascular smooth muscle cell proliferation, neointimal
CC hyperplasia following vessel injury or inflammatory bowel disease or in
CC preventing restenosis and used in prophylaxis. Further diseases/disorders
CC include inflammatory disease, dermatitis, aneurism, arteriosclerosis,
CC atherosclerosis, angitis, cancer or asthma. The AP-1 decoy
CC oligonucleotide with a CDOON is useful to avoid destruction by
CC exonucleases. This sequence represents a circular dumbbell
CC oligodeoxynucleotide related oligo of the invention.
XX
SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 9

ADG43792
ID ADG43792 standard; DNA; 20 BP.

XX AC ADG43792;

XX XX

DT 26-FEB-2004 (first entry)

DE Synthetic NF-kappaB decoy SEQ ID NO:1.

XX NF-kappaB; cerebroprotective; cytostatic; ophthalmological; osteopathic;
KW antiarthritic; antiasthmatic; dermatological; nephrotropic; periodontal;
KW cerebral aneurysm; cancer; Marfan's syndrome; aortic dissection;
KW postangioplastic reconstruction; rheumatoid arthritis; asthma;
KW atopic dermatitis; renal insufficiency; plaque rupture; ss; ets.

XX OS Synthetic.

XX XX WO2003063911-A1.

XX XX 07-AUG-2003.

XX PF 01-FEB-2002; 2002WO-JP000865.

XX XX 01-FEB-2002; 2002WO-JP000865.

XX XX (ANGE-) ANGES MG INC.

XX PI Morishita R, Aoki M, Ogiwara T, Kawasaki T;

XX XX WPI; 2003-748040/70.

XX XX Composition for treating and preventing diseases caused by the expression
PT of gene under regulation of NF-kappaB or ets comprises decoy and carrier.

XX PS Example 2; Page 19; 46pp; Japanese.

XX XX The invention relates to a novel composition for treating and preventing
CC diseases caused by the expression of a gene under the regulation of NF-
CC kappaB or ets comprises at least one decoy and a carrier. A composition
CC of the invention has cerebroprotective, cytosolic, ophthalmological,
CC osteopathic, antiarthritic, antiasthmatic, dermatological, nephrotropic,
CC and periodontal activity. The composition is useful for treating and
CC preventing diseases caused by the expression of a gene under the
CC regulation of NF-kappaB or ets such as cerebral aneurysm, cancer, Marfan's
CC syndrome, aortic dissection, postangioplastic reconstruction, rheumatoid
CC arthritis, asthma, atopic dermatitis, renal insufficiency and plaque
CC rupture. The present sequence represents an NF-kappaB decoy of the
CC invention.

XX XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 10

ADF69631
ID ADF69631 standard; DNA; 20 BP.

XX AC ADF69631;

XX XX 26-FEB-2004 (first entry)

DE NF-kappaB binding site as decoy for inflammatory disease.

XX ss; antiinflammatory; antiarthritic; antirheumatic; antiarteriosclerotic;
KW nephrotropic; inflammatory disease; joint disease;
KW NF-Kappa B binding site; nephritis; hepatitis; renal failure;
KW arteriosclerosis; glomerulonephritis; pyelonephritis; cystitis;
KW prostatitis; urethritis; epididymitis; testitis; arthritis deformans;
KW rheumatoid arthritis; peri-arthritis of shoulder;
KW neck-shoulder-wrist syndrome.

XX OS Homo sapiens.

XX XX WO2003099339-A1.

XX PD 04-DEC-2003.

XX PF 20-MAY-2003; 2003WO-JP006299.

XX XX 29-MAY-2002; 2002JP-00156524.

XX XX (ANGE-) ANGES MG INC.

XX PI Tomita T, Yoshikawa H, Morishita R;

XX XX WPI; 2004-023234/02.

XX XX Remedies or preventing for inflammatory or joint diseases and disorders,
PT e.g. rheumatoid arthritis, arthritis deformans and nephritis, containing
PT decoy of NF-Kappa B or analogous transcriptional factor.

XX PS Disclosure; SEQ ID NO 1; 82pp; Japanese.

XX XX The invention relates to a drug composition for treating or preventing
CC inflammatory or joint disease or disorders comprising at least 1 decoy of
CC NF-Kappa B binding site. The NF-Kappa B decoy is preferably the
CC nucleotide sequence GGATTTCC. The drugs are for inflammatory diseases
CC and disorders, including nephritis, hepatitis, arthritis, acute/chronic
CC renal failure, arteriosclerosis, glomerulonephritis, pyelonephritis,
CC cystitis, prostatitis, urethritis, epididymitis and testitis,
CC particularly arthritis deformans or rheumatoid arthritis, especially
CC rheumatoid arthritis, as well as peri-arthritis of shoulder, neck-shoulder
CC -wrist syndromes and secondary arthritis. This sequence corresponds to
CC the NF-kappaB decoy.

XX SQ Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 1 CCTTGAAGGGATTTCCTCC 20

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us-08-945-805-1.1.rng

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RESULT 11
ADP81765
ID ADM91765 standard; DNA; 20 BP.
XX AC
XX ADM91765;
XX
XX 17-JUN-2004 (first entry)
XX
XX Cis element decoy oligonucleotide #2.
DE transplanted blood vessel; transcription factor; NF Kappa-B; cis element;
XX oligonucleotide; ss.
XX
XX Synthetic.
XX
XX WO2004026342-A1.
XX
XX 01-APR-2004.
XX
XX 27-DEC-2002; 2002WO-JP013805.
XX
XX 20-SEP-2002; 2002JP-00275884.
XX
XX (ANGE-) ANGES MG INC.
XX
XX Sawa Y, Shintani T, Matsuda H;
XX
XX WPI; 2004-295314/27.
XX
XX Method for controlling transcription transplanted blood vessels induced
PT by NF Kappa-B for preventing thickening.
XX
XX Disclosure; SEQ ID NO 2; 31pp; Japanese.
XX
XX The present invention relates to the method for controlling transcription
CC of blood vessels or transplanted blood vessels activated by transcription
CC factor NF Kappa-B by placing them in contact with a decoy against NF
CC Kappa-B. The method is used for preventing thickening in transplanted
CC blood vessels. The present sequence represents a cis element decoy
CC oligonucleotide.
XX
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 12
ADP83986
ID ADP83986 standard; DNA; 20 BP.
XX AC
XX ADP83986;
XX
XX 26-AUG-2004 (first entry)
XX
XX Nuclear factor-kappaB decoy oligonucleotide #1.
XX
XX Nuclear factor-kappaB; NF-kappaB; ets; cerebral aneurysm; cancer;
XX Marfan's syndrome; aortic detachment; post-angioplasty restenosis;
XX chronic articular rheumatism; asthma; atopic dermatitis; nephritis;
XX renal failure; plaque rupture; eosinophilic abnormality; asthma;
XX bronchial asthma; childhood asthma; allergic asthma; atopic asthma;
XX steroid-resistant asthma; SRA; non-allergic asthma; intrinsic asthma;
XX extrinsic asthma; aspirin-induced asthma; cardiac asthma;
XX infectious asthma; allergy; skin disease; mycosis; vaccine; therapy; ss.
XX
XX Unidentified.
XX

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PN XX US2004109843-A1.
XX PD 10-JUN-2004.
XX PF 10-JUL-2003; 2003US-00618362.
XX PR 01-FEB-2002; 2002WO-JP000865.
XX
XX (MORI/) MORISHITA R.
XX (AOKI/) AOKI M.
XX (OGIH/) OGIHARA T.
XX (KAWA/) KAWASAKI T.
XX (MAKI/) MAKINO H.
XX
XX Morishita R, Aoki M, Ogihara T, Kawasaki T, Makino H;
XX WPI; 2004-448815/42.
XX
XX New compositions comprising at least one decoy, useful for the treating
PT and/or preventing a disease, disorder and/or condition caused by
PT expression of a gene controlled by NF-KB or ets, or by eosinophilic
PT abnormality, e.g. cancer.
XX
XX Example 1; SEQ ID NO 1; 37pp; English.
XX
XX The present invention provides a pharmaceutical composition for the
CC treatment and/or prevention of a disease, disorder and/or condition
CC caused by expression of a gene controlled by nuclear factor-kappa B (NF-
CC kappaB) or ets. The invention is useful for treating and preventing
CC disorders and conditions caused by expression of a gene controlled by NF-
CC kappaB or ets such as cerebral aneurysm, cancer, Marfan's syndrome,
CC aortic detachment, post-angioplasty restenosis, nephritis, chronic articular
CC rheumatism, asthma, atopic dermatitis, nephritis, renal failure, and
CC plaque rupture, disorders caused by eosinophilic abnormality such as
CC asthma which includes bronchial asthma, childhood asthma, allergic
CC asthma, atopic asthma, steroid-resistant asthma (SRA), non-allergic
CC cardiac asthma and infectious asthma, allergic diseases, skin diseases
CC and mycosis. The invention is used in the preparation of vaccines. The
CC present sequence is a nuclear factor-kappaB (NF-kappaB) decoy
CC oligonucleotide. This sequence is used in the exemplification of the
XX invention.
XX
XX Sequence 20 BP; 3 A; 7 C; 4 G; 6 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 1 CCTTGAAGGGATTTCCTCC 20

RESULT 13
AAQ90101
ID AAQ90101 standard; DNA; 36 BP.
XX AC
XX AAQ90101;
XX
XX 11-JAN-1996 (first entry)
XX
XX VCAM-1 expression inhibiting oligonucleotide.
XX
XX Vascular cell adhesion molecule; VCAM-1; inhibitory oligonucleotide;
XX transcriptional regulatory factor; diagnosis; treatment; restenosis;
XX atherosclerosis; inflammatory disease; ds.
XX
XX Synthetic.
XX
XX WO9512415-A1.
XX
XX 11-MAY-1995.
XX

```

XX 07-NOV-1994; 94WO-US012797.
 XX
 XX
 PR 05-NOV-1993; 93US-00147878.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA (UYEM-) UNIV EMORY.
 XX
 XX Medford RM, Bennett CF;
 PI WPI; 1995-193802/25.
 XX
 DR Oligo-nucleotide(s) which modulate vascular cell adhesion molecule
 XX expression by binding a transcription regulatory element - used to
 PT diagnose and treat atherosclerosis, restenosis or inflammatory disease.
 PT
 XX
 PS Claim 17; Page 33; 49pp; English.
 XX
 CC AAQ90100-Q90111 bind the vascular cell adhesion molecule (VCAM)-1 gene
 CC transcriptional regulatory factor, therefore inhibiting the expression of
 CC VCAM-1. They can be used in the diagnosis and treatment of restenosis,
 CC atherosclerosis and inflammatory diseases
 XX
 SQ Sequence 36 BP; 3 A; 13 C; 9 G; 11 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAAGGGATTCCCTCC 20
 DB 16 CCTTGAAGGGATTCCCTCC 35
 RESULT 14
 AAQ90100
 ID AAQ90100 standard; DNA; 47 BP.
 XX
 AC AAQ90100;
 XX
 DT 11-JAN-1996 (first entry)
 XX
 DE VCAM-1 expression inhibiting oligonucleotide.
 XX
 KW Vascular cell adhesion molecule; VCAM-1; inhibitory oligonucleotide;
 KW transcriptional regulatory factor; diagnosis; treatment; restenosis;
 KW atherosclerosis; inflammatory disease; ds.
 XX
 OS Synthetic.
 XX
 PN WO9512415-A1.
 XX
 PD 11-MAY-1995.
 XX
 PF 07-NOV-1994; 94WO-US012797.
 XX
 PR 05-NOV-1993; 93US-00147878.
 XX
 PA (ISIS-) ISIS PHARM INC.
 PA (UYEM-) UNIV EMORY.
 XX
 PI Medford RM, Bennett CF;
 XX WPI; 1995-193802/25.
 XX
 DR Oligo-nucleotide(s) which modulate vascular cell adhesion molecule
 XX expression by binding a transcription regulatory element - used to
 PT diagnose and treat atherosclerosis, restenosis or inflammatory disease.
 PT
 XX
 PS Claim 17; Page 33; 49pp; English.
 XX
 CC AAQ90100-Q90111 bind the vascular cell adhesion molecule (VCAM)-1 gene
 CC transcriptional regulatory factor, therefore inhibiting the expression of

CC VCAM-1. They can be used in the diagnosis and treatment of restenosis,
 CC atherosclerosis and inflammatory diseases
 XX
 SQ Sequence 47 BP; 3 A; 17 C; 12 G; 15 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 2.2;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAAGGGATTCCCTCC 20
 DB 22 CCTTGAAGGGATTCCCTCC 41
 RESULT 15
 ACF79417
 ID ACF79417 standard; DNA; 130 BP.
 XX
 AC ACF79417;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE VCAM-1 promoter.
 XX
 KW VCAM-1; promoter; oestrogen; receptor; c-rel; osteoporosis; osteopathic;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT protein_bind 26..35
 FT /*tag= a
 FT /bound_moiety= "Nuclear factor-kappaB"
 FT protein_bind 40..50
 FT /*tag= b
 FT /bound_moiety= "Nuclear factor-kappaB"
 XX
 PN WO2003071281-A2.
 XX
 PD 28-AUG-2003.
 XX
 PF 21-FEB-2003; 2003WO-EP050027.
 XX
 PR 25-FEB-2002; 2002EP-00075789.
 XX
 PA (ALKU) AKZO NOBEL NV.
 XX
 PI Boersma CJC, Van Gool AJ;
 XX WPI; 2003-748205/70.
 XX
 DR Measuring a direct interaction between an estrogen receptor and c-Rel in
 PT an in vitro system, for selecting a compound to treat osteoporosis, by
 PT providing for a detection parameter proportionally related to the degree
 PT of the interaction.
 XX
 PS Example; Page 32; 38pp; English.
 XX
 CC The present sequence in that of a cloned selection of the promoter region
 CC of the VCAM-1 gene. The promoter contains nuclear factor-kappaB response
 CC elements. The invention provides a method to measure a direct interaction
 CC between an estrogen receptor and a transactivation protein (c-Rel) in an
 CC in vitro system by providing for a detection parameter proportionally
 CC related to the degree of the interaction. A yeast two-hybrid assay for
 CC the measurement is provided. The detection parameter, i.e. the method
 CC used to measure the interaction, includes the use of promoter reporter
 CC constructs that contain NF-kappaB or oestrogen receptor responsive
 CC regulatory elements fused to a heterologous reporter gene capable of
 CC signalling the activation of the regulatory element. The method is useful
 CC for selecting a compound for therapeutic efficacy in osteoporosis
 XX
 SQ Sequence 130 BP; 23 A; 43 C; 24 G; 40 T; 0 U; 0 Other;

us-08-945-805-1.rng

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Query Match 100.0%; Score 20; DB 10; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.5; 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTCCCTCC 20
 |||||
 Db 34 CCTTGAAGGGATTCCCTCC 53
 |||||

Search completed: December 28, 2004, 10:15:52
 Job time : 404 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 80 Seconds
(without alignments)
177.697 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgaaggatttcctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	20	100.0	20	4	US-09-166-649B-1
3	20	100.0	36	4	US-08-401-192-2
4	20	100.0	46	4	US-08-401-192-1
5	20	100.0	1032	3	US-08-482-073-8
6	18	90.0	19	4	US-08-401-192-4
7	16.8	84.0	32	4	US-09-474-432B-1507
8	16.8	84.0	32	4	US-09-476-387-1506
9	16.8	84.0	47	4	US-09-474-432B-39
10	16.8	84.0	47	4	US-09-474-432B-40
11	16.8	84.0	47	4	US-09-474-432B-41
12	16.8	84.0	47	4	US-09-474-432B-42
13	16.8	84.0	47	4	US-09-474-432B-43
14	16.8	84.0	47	4	US-09-474-432B-44
15	16.8	84.0	47	4	US-09-474-432B-45
16	16.8	84.0	47	4	US-09-474-432B-46
17	16.8	84.0	47	4	US-09-474-432B-47
18	16.8	84.0	47	4	US-09-474-432B-48
19	16.8	84.0	47	4	US-09-474-432B-49
20	16.8	84.0	47	4	US-09-474-432B-50
21	16.8	84.0	47	4	US-09-474-432B-51
22	16.8	84.0	47	4	US-09-474-432B-52
23	16.8	84.0	47	4	US-09-474-432B-53
24	16.8	84.0	47	4	US-09-474-432B-54
25	16.8	84.0	47	4	US-09-474-432B-55
26	16.8	84.0	47	4	US-09-474-432B-56
27	16.8	84.0	47	4	US-09-474-432B-57

c 28	16.8	84.0	47	4	US-09-474-432B-58	Sequence 58, Appl
c 29	16.8	84.0	47	4	US-09-474-432B-59	Sequence 59, Appl
c 30	16.8	84.0	47	4	US-09-474-432B-60	Sequence 60, Appl
c 31	16.8	84.0	47	4	US-09-474-432B-61	Sequence 61, Appl
c 32	16.8	84.0	47	4	US-09-474-432B-62	Sequence 62, Appl
c 33	16.8	84.0	47	4	US-09-474-432B-63	Sequence 63, Appl
c 34	16.8	84.0	47	4	US-09-474-432B-64	Sequence 64, Appl
c 35	16.8	84.0	47	4	US-09-474-432B-65	Sequence 65, Appl
c 36	16.8	84.0	47	4	US-09-474-432B-66	Sequence 66, Appl
c 37	16.8	84.0	47	4	US-09-474-432B-67	Sequence 67, Appl
c 38	16.8	84.0	47	4	US-09-474-432B-68	Sequence 68, Appl
c 39	16.8	84.0	47	4	US-09-474-432B-69	Sequence 69, Appl
c 40	16.8	84.0	47	4	US-09-474-432B-70	Sequence 70, Appl
c 41	16.8	84.0	47	4	US-09-474-432B-71	Sequence 71, Appl
c 42	16.8	84.0	47	4	US-09-474-432B-72	Sequence 72, Appl
c 43	16.8	84.0	47	4	US-09-474-432B-73	Sequence 73, Appl
c 44	16.8	84.0	47	4	US-09-474-432B-74	Sequence 74, Appl
c 45	16.8	84.0	47	4	US-09-474-432B-75	Sequence 75, Appl

ALIGNMENTS

RESULT 1
US-08-945-805-1
; Sequence 1, Application US/08945805A
; Patent No. 6262033
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, RYUICHI
; APPLICANT: OGIMURA, TOSHIO
; APPLICANT: SUGIMOTO, TOSHIKO
; APPLICANT: MAEDA, KAZUHIRO
; APPLICANT: KAWAMURA, IKUO
; APPLICANT: CHIBA, TOSHIYUKI
; TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB
; FILE REFERENCE: 1993-03CT
; CURRENT APPLICATION NUMBER: US/08/945,805A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/JP96/01234
; EARLIER FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-08-945-805-1

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGATTTCCTCC 20
| | | | | | | | | | | | | | | | | | | | | |
Db 1 CCTTGAAGGATTTCCTCC 20

RESULT 2
US-09-166-649B-1
; Sequence 1, Application US/09166649B
; Patent No. 6753150
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in The City of New York
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBIT
; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/09/166,649B
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 1

عبدالله

;; TITLE OF INVENTION: MOLECULES (ELAMs) AND MOLECULES INVOLVED IN LEUKOCYTE
;; TITLE OF INVENTION: ADHESION (MILAs)
;; NUMBER OF SEQUENCES: 25
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Neave
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: United States of America
;; ZIP: 10020
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/482,073
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,336
;; FILING DATE:
;; APPLICATION NUMBER: US 07/608298
;; FILING DATE: 31-OCT-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/US 90/02357
;; FILING DATE: 27-APR-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/452675
;; FILING DATE: 18-DEC-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/359516
;; FILING DATE: 01-JUN-1989
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/354151
;; FILING DATE: 28-APR-1989
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haley Jr., James F.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: B124CIP4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 596-9000
;; TELEFAX: (212) 596-9090
;; TELEX: 14-8367
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1032 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; US-08-482-073-8

Query Match 100.0%; Score 20; DB 3; Length 1032;
Best Local Similarity 100.0%; Pred. No. 0.25; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 CTTTGAAGGGATTTCCTCC 20
Db 221 CTTTGAAGGGATTTCCTCC 240

RESULT 6
US-08-401-192-4
; Sequence 4, Application US/08401192
; Patent No. 6713621
; GENERAL INFORMATION:
; APPLICANT: Bennett and Medford
; TITLE OF INVENTION: Modulation of selected Gene Expression
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz
; Mackiewicz & No. 6713621ris

;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WORDPERFECT 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/401,192
;; FILING DATE: 09-Mar-1995
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/147,878
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: John W. Caldwell
;; REGISTRATION NUMBER: 28,937
;; REFERENCE/DOCKET NUMBER: ISIS-1021
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19
;; TYPE: Nucleic Acid
;; STRANDEDNESS: Double
;; TOPOLOGY: Linear
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-401-192-4

Query Match 90.0%; Score 18; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 TTGAAGGGATTTCCTCC 20
Db 1 TTGAAGGGATTTCCTCC 18

RESULT 7
US-09-474-432B-1507/c
; Sequence 1507, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1507
; LENGTH: 32
; TYPE: RNA

ORGANISM: Artificial Sequence
FEATURE: Enzymatic Nucleic Acid
NAME/KEY: Description of Artificial Sequence: Enzymatic Nucleic Acid
LOCATION: (2)..(11)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(16)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (24)..(24)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (27)..(29)
OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-474-432B-1507

Query Match 84.0%; Score 16.8; DB 4; Length 32;
Best Local Similarity 90.0%; Pred. No. 6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 20 CCTTGAAGGGAGTTTCCTCC 1

RESULT 8
US-09-476-387-1506/c
Sequence 1506, Application US/09476387
Patent No. 6617438
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka Matulic
APPLICANT: Sweedler, Dave
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleot
FILE REFERENCE: MHB00-831-C (249/073)
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: 09/474,432
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/301,511
PRIOR FILING DATE: 1999-04-28
PRIOR APPLICATION NUMBER: 60/084,866
PRIOR FILING DATE: 1997-11-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1506
LENGTH: 32
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (2)..(11)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(16)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (24)..(24)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (27)..(29)
OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-476-387-1506

ORGANISM: Artificial Sequence
FEATURE: Enzymatic Nucleic Acid
NAME/KEY: Description of Artificial Sequence: Enzymatic Nucleic Acid
LOCATION: (2)..(11)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(16)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (24)..(24)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (27)..(29)
OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-474-432B-39/c

Query Match 84.0%; Score 16.8; DB 4; Length 32;
Best Local Similarity 90.0%; Pred. No. 6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTTCCTCC 20
DB 20 CCTTGAAGGGAGTTTCCTCC 1

RESULT 9
US-09-474-432B-39/c
Sequence 39, Application US/09474432B
Patent No. 6528640
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Beigelman, Leo
APPLICANT: Burgin, Alex
APPLICANT: Beaudry, Amber
APPLICANT: Karpeisky, Alex
APPLICANT: Adamic, Jasenka
APPLICANT: Sweedler, David
APPLICANT: Zinnen, Shawn
TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
FILE REFERENCE: MHB00-831-B (247/276)
CURRENT FILING DATE: 1999-12-19
PRIOR APPLICATION NUMBER: US 60/064,866
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 60/084,727
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 09/186,675
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 09/301,511
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 1526
SOFTWARE: PatentIn version 3.0
SEQ ID NO 39
LENGTH: 47
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (1)..(10)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (12)..(21)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (43)..(47)
OTHER INFORMATION: 2'-O-Methyl
NAME/KEY: misc feature
LOCATION: (22)..(26)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (32)..(32)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (34)..(35)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (37)..(39)
OTHER INFORMATION: 2'-deoxy-2'-amino
NAME/KEY: misc feature
LOCATION: (47)..(47)
OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in
US-09-474-432B-39

Qy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 10
US-09-474-432B-40/c
; Sequence 40, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpelesky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Svedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in a
; US-09-474-432B-40

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 11
US-09-474-432B-41/c
; Sequence 41, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpelesky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Svedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MBH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in a
; US-09-474-432B-41

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 12
US-09-474-432B-42/c
; Sequence 42, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:

us-08-945-805-1.rni

Wed Dec 29 09:34:03 2004

```

; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in
US-09-474-432B-43

Query Match      84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGAGGGAGTTTCCTCC 20
    |||||
Db 30 CTTGAGGGAGTTTCCTCC 11

RESULT 14
US-09-474-432B-44/c
; Sequence 44, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEH00-831-B (247/276)

```

```

; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEH00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxybasic moiety, in a
US-09-474-432B-42

Query Match      84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTTGAGGGAGTTTCCTCC 20
    |||||
Db 30 CTTGAGGGAGTTTCCTCC 11

RESULT 13
US-09-474-432B-43/c
; Sequence 43, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Karpeisky, Alex

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; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxyabasic moiety, in a

US-09-474-432B-44

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

RESULT 15

US-09-474-432B-45/c
; Sequence 45, Application US/09474432B
; Patent No. 6528640
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Beigelman, Leo
; APPLICANT: Burgin, Alex
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka
; APPLICANT: Sweedler, David
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide triphosphate and their incorporation into oligonucleot
; FILE REFERENCE: MEHB00-831-B (247/276)
; CURRENT APPLICATION NUMBER: US/09/474,432B
; CURRENT FILING DATE: 1999-12-19
; PRIOR APPLICATION NUMBER: US 60/064,866
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: US 60/084,727

; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: US 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: US 09/301,511
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 1526
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 47
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(21)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (43)..(47)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (22)..(26)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (32)..(32)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (34)..(35)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (37)..(39)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (47)..(47)
; OTHER INFORMATION: 3'-end phosphate attached to an inverted deoxyabasic moiety, in a

US-09-474-432B-45

Query Match 84.0%; Score 16.8; DB 4; Length 47;
Best Local Similarity 90.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCTTGAAGGGATTTCCTCC 20
|||||
Db 30 CCTTGAAGGGATTTCCTCC 11

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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 10:09:11 ; Search time 3939 Seconds
(without alignments)
28.272 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgaaggattccctcc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4105333 seqs, 2784095677 residues

Total number of hits satisfying chosen parameters: 8210666

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

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11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	20	100.0	20	9	US-09-832-841-1
2	20	100.0	20	10	US-09-937-839-1
3	20	100.0	20	10	US-09-166-649B-1
4	20	100.0	20	16	US-10-466-239-1
5	20	100.0	20	17	US-10-618-362A-1
6	20	100.0	20	17	US-10-618-362A-14
7	20	100.0	20	17	US-10-783-635-1
8	20	100.0	20	17	US-10-366-718-1
9	20	100.0	20	17	US-10-468-717-1
10	20	100.0	20	18	US-10-824-757-1
11	20	100.0	1032	15	US-10-234-041-9
12	18	90.0	554	16	US-10-424-599-51726

C 13	17	85.0	708	16	US-10-343-650A-97	Sequence 97, Appl
C 14	16.8	84.0	32	10	US-09-825-805-1548	Sequence 1548, Ap
C 15	16.8	84.0	40	10	US-09-916-466-399	Sequence 399, App
C 16	16.8	84.0	40	10	US-09-916-466-400	Sequence 400, App
C 17	16.8	84.0	40	10	US-09-916-466-401	Sequence 401, App
C 18	16.8	84.0	40	10	US-09-916-466-402	Sequence 402, App
C 19	16.8	84.0	40	10	US-09-916-466-403	Sequence 403, App
C 20	16.8	84.0	40	10	US-09-916-466-404	Sequence 404, App
C 21	16.8	84.0	40	10	US-09-916-466-405	Sequence 405, App
C 22	16.8	84.0	40	10	US-09-916-466-406	Sequence 406, App
C 23	16.8	84.0	40	10	US-09-916-466-407	Sequence 407, App
C 24	16.8	84.0	40	10	US-09-916-466-408	Sequence 408, App
C 25	16.8	84.0	40	10	US-09-916-466-409	Sequence 409, App
C 26	16.8	84.0	40	10	US-09-916-466-410	Sequence 410, App
C 27	16.8	84.0	40	10	US-09-916-466-411	Sequence 411, App
C 28	16.8	84.0	40	10	US-09-916-466-412	Sequence 412, App
C 29	16.8	84.0	40	10	US-09-916-466-413	Sequence 413, App
C 30	16.8	84.0	40	10	US-09-916-466-414	Sequence 414, App
C 31	16.8	84.0	40	10	US-09-916-466-415	Sequence 415, App
C 32	16.8	84.0	40	10	US-09-916-466-416	Sequence 416, App
C 33	16.8	84.0	40	10	US-09-916-466-417	Sequence 417, App
C 34	16.8	84.0	40	10	US-09-916-466-418	Sequence 418, App
C 35	16.8	84.0	40	10	US-09-916-466-419	Sequence 419, App
C 36	16.8	84.0	40	10	US-09-916-466-420	Sequence 420, App
C 37	16.8	84.0	40	10	US-09-916-466-421	Sequence 421, App
C 38	16.8	84.0	40	10	US-09-916-466-422	Sequence 422, App
C 39	16.8	84.0	40	10	US-09-916-466-423	Sequence 423, App
C 40	16.8	84.0	40	10	US-09-916-466-424	Sequence 424, App
C 41	16.8	84.0	40	10	US-09-916-466-425	Sequence 425, App
C 42	16.8	84.0	40	10	US-09-916-466-426	Sequence 426, App
C 43	16.8	84.0	40	10	US-09-916-466-427	Sequence 427, App
C 44	16.8	84.0	40	10	US-09-916-466-428	Sequence 428, App
C 45	16.8	84.0	40	10	US-09-916-466-429	Sequence 429, App

ALIGNMENTS

RESULT 1

US-09-832-841-1

Sequence 1, Application US/09832841

Patent No. US20020098162A1

GENERAL INFORMATION:

APPLICANT: MORISHITA, RYUICHI

APPLICANT: OGIMURA, TOSHIO

APPLICANT: SUGIMOTO, TOSHIKO

APPLICANT: MAEDA, KAZUHIRO

APPLICANT: KAWAMURA, IKUO

APPLICANT: CHIBA, TOSHIYUKI

TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB

FILE REFERENCE: 18993-OPCT

CURRENT APPLICATION NUMBER: US/09/832,841

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: 08/945,805

PRIOR FILING DATE: 1998-01-06

PRIOR APPLICATION NUMBER: PCT/JP96/01234

PRIOR FILING DATE: 1996-05-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 20

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA

US-09-832-841-1

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGATTCCCTCC 20
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us-08-945-805-1.1.rnpb

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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 2
US-09-937-839-1
; Sequence 1, Application US/09937839
; Publication No. US20030013195A1
; GENERAL INFORMATION:
; APPLICANT: Kaneda, Yasufumi
; TITLE OF INVENTION: Virus Envelope Vector for Gene Transfer
; FILE REFERENCE: 59150-8010
; CURRENT APPLICATION NUMBER: US/09/937.839
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/JP01/00782
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: JP 2000-25596
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-09-937-839-1

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 3
US-09-166-649B-1
; Sequence 1, Application US/09166649B
; Publication No. US20030087302A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in The City of New York
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING
; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/09/166.649B
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: Primer Against Human NF-KB
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: PCR Primer Against Human NF-KB
US-09-166-649B-1

Query Match      100.0%; Score 20; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 4
US-10-466-239-1
; Sequence 1, Application US/10466239
; Publication No. US20040072726A1
; GENERAL INFORMATION:
; APPLICANT: Ryuchi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Tomio Kawasaki
; TITLE OF INVENTION: Decoy-containing pharmaceutical compositions and method of using
; FILE REFERENCE: ANGES-1 US
; CURRENT APPLICATION NUMBER: US/10/466.239
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: PCT/JP02/00865
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NF-?B decoy
; PUBLICATION INFORMATION:
US-10-466-239-1

Query Match      100.0%; Score 20; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 5
US-10-618-362A-1
; Sequence 1, Application US/10618362A
; Publication No. US20040109843A1
; GENERAL INFORMATION:
; APPLICANT: Ryuchi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Tomio Kawasaki
; APPLICANT: Hirofumi Makino
; TITLE OF INVENTION: Pharmaceutical composition containing decoy and use of the same
; FILE REFERENCE: ANGES-1 CIP US
; CURRENT APPLICATION NUMBER: US/10/618.362A
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: PCT/JP02/00865
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappaB Decoy
US-10-618-362A-1

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
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Db      1  CCTTGAAGGGATTTCCTCC 20

RESULT 6
US-10-618-362A-14/c

Query Match      100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CCTTGAAGGGATTTCCTCC 20
      |||
Db      1  CCTTGAAGGGATTTCCTCC 20
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; Sequence 14, Application US/10618362A
; Publication No. US20040109843A1
; GENERAL INFORMATION:
; APPLICANT: Ryuichi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Tomio Kawasaki
; APPLICANT: Hirofumi Makino
; TITLE OF INVENTION: Pharmaceutical composition containing decoy and use of the same
; FILE REFERENCE: ANGES-1 CIP US
; CURRENT APPLICATION NUMBER: US/10/618.362A
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: PCT/JP02/00865
; PRIOR FILING DATE: 2002-02-01
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappaB Decoy
US-10-618-362A-14

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 20 CCTTGAAGGGATTTCCTCC 1

RESULT 7

US-10-783-635-1
; Sequence 1, Application US/10783635
; Publication No. US20040142391A1
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University in The City of New York
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David M
; TITLE OF INVENTION: METHODS FOR DETERMINING WHETHER A COMPOUND IS CAPABLE OF INHIBITING
; FILE REFERENCE: 56613
; CURRENT APPLICATION NUMBER: US/10/783.635
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: US/09/166,649
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: Primer Against Human NF-kB
; FEATURE:
; NAME/KEY: Primer
; LOCATION: (1)..(20)
; OTHER INFORMATION: PCR Primer Against Human NF-kB
US-10-783-635-1

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 8
US-10-366-718-1
; Sequence 1, Application US/10366718
; Publication No. US20040162250A1
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, RYUICHI
; APPLICANT: OGIWARA, TOSHIO
; APPLICANT: SUGIMOTO, TOSHIKO
; APPLICANT: MAEDA, KAZUHIRO
; APPLICANT: KAWAMURA, IKUO
; APPLICANT: CHIBA, TOSHIYUKI
; TITLE OF INVENTION: REMEDY AND PREVENTIVE FOR DISEASES CAUSED BY NF-KB
; FILE REFERENCE: 18993-OPCT
; CURRENT APPLICATION NUMBER: US/10/366,718
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US/09/832,841
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 08/945,805
; PRIOR FILING DATE: 1998-01-06
; PRIOR APPLICATION NUMBER: PCT/JP96/01234
; PRIOR FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-366-718-1

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 1 CCTTGAAGGGATTTCCTCC 20

RESULT 9

US-10-468-717-1
; Sequence 1, Application US/10468717
; Publication No. US20040162251A1
; GENERAL INFORMATION:
; APPLICANT: Ryuichi Morishita
; APPLICANT: Motokuni Aoki
; APPLICANT: Toshio Ogiwara
; APPLICANT: Yasufumi Kaneda
; APPLICANT: Hiroshige Nakamura
; TITLE OF INVENTION: Pharmaceutical composition containing decoy and method of using t
; FILE REFERENCE: ANGES-2 US
; CURRENT APPLICATION NUMBER: US/10/468,717
; CURRENT FILING DATE: 2003-08-20
; PRIOR APPLICATION NUMBER: PCT/JP02/00990
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 2001-44350
; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NF-kappaB Decoy
US-10-468-717-1

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-08-945-805-1.rnpb

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; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-234-041-9

Query Match
Best Local Similarity 100.0%; Score 20; DB 15; Length 1032;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGGATTTCCCTCC 20
Db 221 CCTTGAAGGGGATTTCCCTCC 240

RESULT 12
US-10-424-599-51726
; Sequence 51726, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 51726
; LENGTH: 554
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_17722C.1
US-10-424-599-51726

Query Match
Best Local Similarity 90.0%; Score 18; DB 16; Length 554;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGGATTTCCCT 18
Db 421 CCTTGAAGGGGATTTCCCT 438

RESULT 13
US-10-343-650A-97/c
; Sequence 97, Application US/10343650A
; Publication No. US20040067499A1
; GENERAL INFORMATION:
; APPLICANT: HAGA, TATSUYA
; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: 31671-186347
; CURRENT APPLICATION NUMBER: US/10/343,650A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: JP 2000/237818
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: JP 2001/34434
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 694
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 708
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(708)
US-10-343-650A-97

Query Match
Best Local Similarity 85.0%; Score 17; DB 16; Length 708;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGGATTTCCCTCC 20
Db 221 CCTTGAAGGGGATTTCCCTCC 240

RESULT 10
US-10-824-757-1
; Sequence 1, Application US/10824757
; Publication No. US20040219674A1
; GENERAL INFORMATION:
; APPLICANT: Kaneda, Yasufumi
; TITLE OF INVENTION: Virus Envelope Vector for Gene Transfer
; FILE REFERENCE: 59150-8010
; CURRENT APPLICATION NUMBER: US/10/824,757
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/937,839
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: PCT/JP01/00782
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: JP 2000-25596
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide
US-10-824-757-1

Query Match
Best Local Similarity 100.0%; Score 20; DB 18; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGGATTTCCCTCC 20
Db 1 CCTTGAAGGGGATTTCCCTCC 20

RESULT 11
US-10-234-041-9
; Sequence 9, Application US/10234041
; Publication No. US20030153731A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Hession, Catherine A.
; APPLICANT: Lobb, Roy R.
; APPLICANT: Goelz, Susan E.
; APPLICANT: Osborn, Laurelee
; APPLICANT: Benjamin, Christopher D.
; APPLICANT: Rosa, Margaret D.
; TITLE OF INVENTION: Endothelial Cell-Leukocyte Adhesion
; TITLE OF INVENTION: Molecules (ELAMs) and Molecules Involved in Leukocyte
; TITLE OF INVENTION: Adhesion (MILAG)
; FILE REFERENCE: B124CP2DV2CN
; CURRENT APPLICATION NUMBER: US/10/234,041
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 08/473,764
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/342,642
; PRIOR FILING DATE: 1994-11-21
; PRIOR APPLICATION NUMBER: 07/608,298
; PRIOR FILING DATE: 1990-10-31
; PRIOR APPLICATION NUMBER: 07/452,675
; PRIOR FILING DATE: 1989-12-18
; PRIOR APPLICATION NUMBER: 07/359,516
; PRIOR FILING DATE: 1989-06-01
; PRIOR APPLICATION NUMBER: 07/345,151
; PRIOR FILING DATE: 1989-04-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9

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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 17
Db 562 CCTTGAAGGGATTTCCTCC 546

RESULT 14
US-09-825-805-1548/c
; Sequence 1548, Application US/09825805
; Publication No. US20030004122A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Belgelman, Leo
; APPLICANT: Beaudry, Amber
; APPLICANT: Karpeisky, Alex
; APPLICANT: Adamic, Jasenka Matulic
; APPLICANT: Sweedler, Dave
; APPLICANT: Zinnen, Shawn
; TITLE OF INVENTION: Nucleotide Triphosphate and their Incorporation into Oligonucleotides
; FILE REFERENCE: MBHB00-831-F (400/009)
; CURRENT APPLICATION NUMBER: US/09/825,805
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/578,223
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 09/476,387
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 09/474,432
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/301,511
; PRIOR FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: 09/186,675
; PRIOR FILING DATE: 1998-11-04
; PRIOR APPLICATION NUMBER: 60/083,727
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/064,866
; PRIOR FILING DATE: 1997-11-05
; NUMBER OF SEQ ID NOS: 1558
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1548
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (2)..(11)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(16)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (24)..(24)
; OTHER INFORMATION: 2'-deoxy-2'-amino
; NAME/KEY: misc_feature
; LOCATION: (27)..(29)
; OTHER INFORMATION: 2'-deoxy-2'-amino
US-09-825-805-1548

Query Match 84.0%; Score 16.8; DB 10; Length 32;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 20 CCTTGAAGGGATTTCCTCC 1

RESULT 15
US-09-916-466-399/c
; Sequence 399, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
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; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 399
; LENGTH: 40
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid Molecules
US-09-916-466-399

Query Match 84.0%; Score 16.8; DB 10; Length 40;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCTTGAAGGGATTTCCTCC 20
Db 24 CCTTGAAGGGATTTCCTCC 5

Search completed: December 28, 2004, 13:15:13
Job time : 3940 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2004, 07:31:07 ; Search time 2988 Seconds
(without alignments)
243.907 Million cell updates/sec

Title: US-08-945-805-1

Perfect score: 20

Sequence: 1 ccttgaaggattccctcc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gse1:*
9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	334	5	BY150286
2	20	100.0	701	2	BF385710
3	20	100.0	768	9	CR139070 Reverse s
4	18	90.0	504	7	CO695591
5	18	90.0	604	8	CL133636
6	18	90.0	627	5	BW242276
7	17.4	87.0	269	2	BB002216
8	17.4	87.0	453	6	CA857737
9	17.4	87.0	478	4	BX072801
10	17.4	87.0	529	5	BX844476
11	17.4	87.0	580	4	BM179747
12	17.4	87.0	606	7	CR585617
13	17.4	87.0	671	5	BX850643
14	17.4	87.0	885	6	CD303290
15	17.4	87.0	938	8	CC091597
16	17.4	87.0	1146	4	BG531353
17	17.4	87.0	1172	8	CC239703
18	17.4	87.0	1172	8	CC302265
19	17	85.0	350	7	R25866
20	17	85.0	512	2	BB755468
21	17	85.0	831	4	BI870073
22	16.8	84.0	152	2	BB064146
23	16.8	84.0	202	9	CG632344
24	16.8	84.0	246	2	AW571808

c	25	16.8	84.0	258	2	AW190931
c	26	16.8	84.0	265	1	AI367826
c	27	16.8	84.0	294	5	BQ102591
c	28	16.8	84.0	306	8	AZ480348
c	29	16.8	84.0	371	1	AA775085
c	30	16.8	84.0	376	1	AA055416
c	31	16.8	84.0	377	5	BY583522
c	32	16.8	84.0	397	8	CC178434
c	33	16.8	84.0	405	2	BF038388
c	34	16.8	84.0	413	8	AZ429984
c	35	16.8	84.0	426	7	H02051
c	36	16.8	84.0	430	5	BY482479
c	37	16.8	84.0	436	7	T93077
c	38	16.8	84.0	446	7	CO298103
c	39	16.8	84.0	455	9	CE433772
c	40	16.8	84.0	466	1	AA054954
c	41	16.8	84.0	468	6	BY661708
c	42	16.8	84.0	478	8	BH098047
c	43	16.8	84.0	491	6	CF166444
c	44	16.8	84.0	496	1	AA624941
c	45	16.8	84.0	504	6	CA654764

ALIGNMENTS

RESULT 1

BY150286

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY150286 334 bp mRNA linear EST 10-DEC-2002
BY150286 RIKEN full-length enriched, 17, 5 days embryo whole body
Mus musculus cDNA clone U30275P17 5', mRNA sequence.

BY150286

BY150286.1 GI:26286815

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 334)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, Y., Osato, N., Saito, R., Suzuki, H., Yamana, H.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusio, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalia, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Griboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Kongsaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Varaldo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sakaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

CONTACT: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: L1AM9534 row: c column: 18
 High quality sequence stop: 699.
 Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4196681"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP L19"
 /note="Organ: Liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

FEATURES

source

ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 701;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAAGGGATTCCCTCC 20
 |||||
 DB 162 CCTTGAAGGGATTCCCTCC 181

RESULT 3

CR139070 768 bp DNA linear GSS 06-JUL-2004
 LOCUS Reverse strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHPP137g11, genomic survey sequence.
 DEFINITION
 CR139070
 CR139070.1 GI:49886797
 GSS; genome survey sequence; MICE.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 768)
 Adams D.J., Biggs P.J., Cox A.V., Davies R.M., van der Weyden L., Jonkers J., Smith J., Plumb R.W., Taylor R.G., Nishijima I., Yu Y., Rogers J. and Bradley A.
 REFERENCE Direct Submission
 AUTHORS Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, UK. <http://www.sanger.ac.uk/MICE>
 TITLE CB10 1SA, UK.
 JOURNAL
 FEATURES
 Location/Qualifiers
 1..768
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPP137g11"
 /clone_lib="MHPP"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCTTGAAGGGATTCCCTCC 20
 |||||
 DB 636 CCTTGAAGGGATTCCCTCC 655

RESULT 4

CO695591 504 bp mRNA linear EST 26-JUL-2004
 LOCUS DG11-87k18 DG11-kidney Canis familiaris cDNA 3', mRNA sequence.
 DEFINITION
 CO695591
 ACCESSION
 VERSION CO695591.1 GI:50644257

Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
 Aizawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Hirozane T., Imotani K., Ishii Y., Itoh M., Kawai J., Konno H., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Sakai K., Sakazume N., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Waki K., Watanabe A., Muramatsu M. and Hayashizaki Y. Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome cDNA library project of Genome Exploration Research Group in Riken
 Encyclopaedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN
 Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source

Location/Qualifiers
 1..334
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="L930275P17"
 /tissue="whole body"
 /dev_stage="17.5 days embryo"
 /clone_lib="RIKEN full-length enriched, 17.5 days embryo whole body"

ORIGIN

Query Match 100.0%; Score 20; DB 5; Length 334;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTCCCTCC 20
 |||||

DB 199 CCTTGAAGGGATTCCCTCC 218

RESULT 2

BF385710 701 bp mRNA linear EST 27-NOV-2000
 LOCUS 602047366F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4196681 5', mRNA sequence.

DEFINITION

BF385710.1 GI:11367015

ACCESSION

EST.

KEYWORDS

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 701)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

KEYWORDS
SOURCE  EST.
ORGANISM  Canis familiaris (dog)
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS  Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE  1 (bases 1 to 504)
JOURNAL  Schluter, J., Hermans, J., Weindel, M., Schuette, D., Kranz, H.,
COMMENT  Henrich, J., and Loebbert, R.
        Dog arrayTAG cDNA clone collection
        Contact: Thomas Schluter
        LION bioscience AG
        Walhoferstrasse 98, D-69123 Heidelberg, Germany
        Tel: +49 6221 4038 150
        Fax: +49 6221 4038 290
        Email: Thomas.Schluter@lionbioscience.com.
FEATURES
Source  Location/Qualifiers
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        /organism="Canis familiaris"
        /mol_type="mRNA"
        /strain="Beagle"
        /db_xref="taxon:9615"
        /tissue_type="kidney"
        /dev_stage="adult"
        /lab_host="DH10B"
        /clone_lib="DGI1-kidney"
        /note="Organ: kidney; Vector: Dog pBluescript LION"
ORIGIN
Query Match 90.0%; Score 18; DB 7; Length 504;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 TTGAAGGGATTTCCTCC 20
Db 440 TTGAAGGGATTTCCTCC 457
RESULT 5
CC133636/c
LOCUS 604 bp DNA linear GSS 16-APR-2003
DEFINITION NDL.80H15.T7 Notre Dame Liverpool Aedes aegypti genomic clone
ACCESSION CC133636
VERSION NDL.80H15, genomic survey sequence.
KEYWORDS CC133636.1 GI:30002691
SOURCE GSS.
ORGANISM Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.
REFERENCE 1 (bases 1 to 604)
AUTHORS Loftus, B., Shetty, J., Knudson, D. and Severson, D.
TITLE BAC end sequencing of Aedes aegypti
JOURNAL Unpublished (2003)
COMMENT Other GSSs: NDL.80H15.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
FEATURES
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/clone_lib="Notre Dame Liverpool"
/note="vector: pECBAC1; Site 1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
ORIGIN
Query Match 90.0%; Score 18; DB 8; Length 604;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCTTGAGGGATTTCCTC 18
Db 159 CCTTGAGGGATTTCCTC 142
RESULT 6
BW242276/c
LOCUS 527 bp mRNA linear EST 09-NOV-2002
DEFINITION BW242276 Nori Satoh unpublished cDNA library, tailbud embryo Ciona
intestinalis cDNA clone citb10ln15 5', mRNA sequence.
ACCESSION BW242276
VERSION BW242276.1 GI:24822194
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
REFERENCE 1 (bases 1 to 627)
AUTHORS Satou, Y., Shin-i, T., Kohara, Y. and Satoh, N.
TITLE Expressed genes in Ciona intestinalis (2002c)
JOURNAL Unpublished (2002)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Kyoto-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
Source  Location/Qualifiers
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        /tissue_type="whole animal"
        /dev_stage="tailbud embryo"
        /clone_lib="Nori Satoh unpublished cDNA library, tailbud
        embryo"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CTTGAAGGGATTTCCTC 19
Db 451 CTTGAAGGGATTTCCTC 434
RESULT 7
BB002216
LOCUS 269 bp mRNA linear EST 22-JUN-2000
DEFINITION BB002216 RIKEN full-length enriched, 0 day neonate skin Mus
musculus cDNA clone 4631430K12 3' similar to D80005 Human mRNA for
KIAA0183 gene, mRNA sequence.
ACCESSION BB002216
VERSION BB002216.1 GI:8091661
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

1. (bases 1 to 269)
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T.,
 Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
 Iizawa,M., Kadoya,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
 Kiyosawa,H., Koijima,Y., Kondo,S., Koya,S., Kurihara,C.,
 Kusakabe,M., Matsuyama,T., Miki,R., Munono,Y., Nakamura,M., Oda,H.,
 Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,C.,
 Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,
 Takanashi,F., Tominaga,N., Toyota,T., Tsunoda,Y., Watahiki,A.,
 Watanabe,S., Yamamura,T., Yamana,I., Yano,R., Yasunishi,A.,
 Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and
 Hayashizaki,Y.
 RIKEN Mouse ESTs (Konno,H., et al.)
 Unpublished (2000)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome.res@sc.riken.jp, URL:http://genome.gsc.riken.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S.,
 Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by
 trehalose and its application for the synthesis of full length
 cDNA. Proc. Natl. Acad. Sci. U.S.A. 95(2) 520-524 (1998)
 Itoh,M., Kitsuura,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
 Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
 Okazaki,Y. and Hayashizaki,Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 source
 1. 269
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
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 /clone="4631430K12"
 /sex="mixed"
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 /dev stage="0 day neonate"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, 0 day neonate
 skin"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGAGATCTCGAGCTCTTTTCTTTTCTTATN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. cDNA went through one round of normalization
 to Rot = 10.0 and subtracted to Rot = 100.0. Second
 strand cDNA was prepared with the primer adapter of
 sequence [5' GAGAGAGAGATCTCGAGTAAATTAATATCCCCCCCCCCCC
 3']. cDNA was cloned into the XhoI and BamHI sites.
 Vector: a modified pBluescript KS(+) after bulk excision
 from Lambda FLC I"

ORIGIN
 Query Match 87.0%; Score 17.4; DB 2; Length 269;
 Total similarity 94.7%; Pred. No. 7.2e+02;

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RESULT 9
BX844476/c
LOCUS
DEFINITION
  BJ072801 NIBB Mochii normalized Xenopus tailbud library Xenopus
  laevis cDNA clone XL099p17 5', mRNA sequence.
ACCESSION
  BJ072801
VERSION
  BJ072801.1 GI:17502990
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 478)
  Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
  Kohara,Y.
  Expressed genes in X. laevis embryo
  Unpublished (2001)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp
  The information of this clone is available through the following
  URL.
  http://xenopus.nibb.ac.jp.
FEATURES
  source
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        /clone_lib="NIBB Mochii normalized Xenopus tailbud
        library"
ORIGIN
  Query Match 87.0%; Score 17.4; DB 4; Length 478;
  Best Local Similarity 94.7%; Pred. No. 7.9e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 2 CTTGAAGGGATTCCCTCC 20
  |||||
  Db 336 CTTGAAGGGATTCCCTCC 318

RESULT 10
BX844476/c
LOCUS
DEFINITION
  BX844476 NICHG XGC Emb1 Xenopus laevis cDNA clone IMAGE:4959036
  ; IMAGE:6633714 5', mRNA sequence.
ACCESSION
  BX844476
VERSION
  BX844476.1 GI:39734522
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 529)
  Heil,O., Neubert,P., Petera,M., Radelof,U., Schneider,D.,
  Schroth,A., Korn,B. and Landgrebe,J.
  Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
  Unpublished (2003)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
  RZPD; IMAGE:4959036.
  RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB

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No.998) http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi?response?libNo=998 RZPDLIB; Xenopus
laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
bin/products/showLib.pl.cgi?response?libNo=988 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
SP6, 5' ATTAGGTGACACTATAG 3'.
FEATURES
  source
    Location/Qualifiers
      1..529
        /organism="Xenopus laevis"
        /mol_type="mRNA"
        /db_xref="taxon:8355"
        /clone="IMAGE:998B1814205 ; IMAGE:6633714"
        /tissue_type="embryo (stage 10)"
        /lab_host="DH10B (phage-resistant)"
        /clone_lib="NICHG XGC Emb1"
        /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
        Cloned unidirectionally. Primer: Oligo dT. Average insert
        size 1.55 kb. Constructed by Life Technologies. Note: This
        is a Xenopus Gene Collection (XGC) library."
ORIGIN
  Query Match 87.0%; Score 17.4; DB 5; Length 529;
  Best Local Similarity 94.7%; Pred. No. 8e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 2 CTTGAAGGGATTCCCTCC 20
  |||||
  Db 182 CTTGAAGGGATTCCCTCC 164

RESULT 11
BM179747/c
LOCUS
DEFINITION
  BM179747 Y1 NICHG XGC Emb4 Xenopus laevis cDNA clone IMAGE:4959036
  5', similar to FR:095197 095197 RETICULON PROTEIN. ;, mRNA sequence.
ACCESSION
  BM179747
VERSION
  BM179747.1 GI:17403818
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
  Xenopodinae; Xenopus; Xenopus.
REFERENCE
  1 (bases 1 to 580)
  NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Other ESTs: da11d07.xl
  Contact: Robert Strausberg, Ph.D.
  Email: cgapsb-r@mail.nih.gov
  Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: Xenopus clones from this library are available
  through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
  Seq primer: -40RP from Gibco
  High quality sequence stop: 442.
FEATURES
  source
    Location/Qualifiers
      1..580
        /organism="Xenopus laevis"
        /mol_type="mRNA"
        /db_xref="taxon:8355"
        /clone="IMAGE:4959036"
        /dev_stage="embryo, stage 31-32"
        /lab_host="DH10B (phage-resistant)"

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/clone_lib="NICHDP_XGC_Emb4"
/notes="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN
  Query Match      87.0%; Score 17.4; DB 4; Length 580;
  Best Local Similarity 94.7%; Pred. No. 8.2e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTTGAAGGGATTCCCTCC 20
    |||||
DB 346 CTTGAAGGGATGTCCTCC 328

RESULT 12
CRS85617/c
LOCUS
DEFINITION
  606 bp mRNA linear EST 26-JUL-2004
  CRS85617 XGC-tailbud-head Xenopus tropicalis cDNA clone THDA052j02
  3', mRNA sequence.
ACCESSION
  CRS85617
  CRS85617.1 GI:50585617
KEYWORDS
  EST.
SOURCE
  Xenopus tropicalis (western clawed frog)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
  Xenopodinae; Xenopus; Silurana.

REFERENCE
  1 (bases 1 to 606)
  Croning M.D.R., Ashurst J.L., Taylor R., Garrett N. and Rogers J.
  Sanger Xenopus tropicalis EST project 2001 (2004)
  Unpublished (2004)
  Contact: Croning MDR
  Sanger Institute
  Hinxton, Cambridgeshire, CB10 1SA, UK
  Email: tropesanger.ac.uk
  Sanger Xenopus tropicalis EST project 2001
  TROPICALIS SEQUENCE ID: THDA052j02.q1k77
  This sequence is from a Xenopus Gene Collection (XGC) library
  constructed by Nigel Garrett.
  Seq primer: T7.
  Location/Qualifiers
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    /organism="Xenopus tropicalis"
    /mol_type="mRNA"
    /db_xref="taxon:8364"
    /clone="THDA052j02"
    /dev_stage="tailbud head (stage 28-30)"
    /lab_host="Escherichia coli DH10B."
    /clone_lib="XGC-tailbud-head"
    /note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
    was oligo dT primed from 5ug of poly A+ RNA from tailbud
    head. EcoRI-NotI cut cDNA was then ligated into pCS107
    with EcoRI at the 5' end and NotI at the 3' end."

ORIGIN
  Query Match      87.0%; Score 17.4; DB 7; Length 606;
  Best Local Similarity 94.7%; Pred. No. 8.2e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTTGAAGGGATTCCCTC 19
    |||||
DB 543 CCTTGAAGGGATTCCCG 525

RESULT 13
BX850643/c
LOCUS
DEFINITION
  671 bp mRNA linear EST 11-DEC-2003
  BX850643 NICHDP_XGC_Emb4 Xenopus laevis cDNA clone IMAGp998H1310927
  ; IMAGE:4959036 5', mRNA sequence.
ACCESSION
  BX850643

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VERSION
KEYWORDS
SOURCE
ORGANISM
  Xenopus laevis (African clawed frog)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
  Xenopodinae; Xenopus;
  1 (bases 1 to 671)
  Heil, O., Neubert, P., Peters, M., Radelof, U., Schneider, D.,
  Schroth, A., Korn, B. and Landgrebe, J.
  Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
  Unpublished (2003)
  Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
  RZPD; IMAGp998H1310927.
  RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
  No.988) http://www.rzpd.de/cgi-
  bin/products/showlib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
  laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
  bin/products/showlib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
  RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
  Heubnerweg 6, D-14059 Berlin, Germany
  Tel: +49 30 32639 101
  Fax: +49 30 32639 111
  www.rzpd.de
  This clone is available royalty-free from RZPD;
  contact RZPD (clone@rzpd.de) for further information. Seq primer:
  SP6, 5' ATTTAGTGTGACATATAG 3'.
  Location/Qualifiers
    1..671
    /organism="Xenopus laevis"
    /mol_type="mRNA"
    /db_xref="taxon:8355"
    /clone="IMAGp998H1310927 ; IMAGE:4959036"
    /dev_stage="embryo, stage 31-32"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NICHDP_XGC_Emb4"
    /note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
    NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
    dT. Average insert size 2.1 kb. Constructed by Life
    Technologies. Note: This is a Xenopus Gene Collection
    (XGC) library."

ORIGIN
  Query Match      87.0%; Score 17.4; DB 5; Length 671;
  Best Local Similarity 94.7%; Pred. No. 8.4e+02;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CTTGAAGGGATTCCCTCC 20
    |||||
DB 348 CTTGAAGGGATGTCCTCC 330

RESULT 14
CD303290/c
LOCUS
DEFINITION
  885 bp mRNA linear EST 27-MAY-2003
  AGENCOURT 14233231 NICHDP_XGC_Brn1 Xenopus laevis cDNA clone
  IMAGE:6955529 5', mRNA sequence.
ACCESSION
  CD303290
  CD303290.1 GI:31083109
KEYWORDS
  EST.
SOURCE
  Xenopus laevis (African clawed frog)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
  Xenopodinae; Xenopus;
  1 (bases 1 to 885)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics

```


National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement:

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>

Plate: LLAM14581 Row: c column: 16
High quality sequence stop: 687.
Location/Qualifiers

FEATURES

1. .885
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8155"
/clone="IMAGE:6955529"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC Brn1"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 885;
Best Local Similarity 94.7%; Pred. No. 8.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CTTGAAGGGATTCCCTCC 20
|||||
Db 337 CTTGAAGGGATTCCCTCC 319

RESULT 15

CC091597
LOCUS
DEFINITION CSU-K33r.24N21.T7 CSU-K33r Aedes aegypti genomic clone
CSU-K33r.24N21, genomic survey sequence.

CC091597
VERSION CC091597.1 GI:29950049
KEYWORDS GSS.

SOURCE
ORGANISM Aedes aegypti (yellow fever mosquito)
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.

REFERENCE
AUTHORS 1 (bases 1 to 938)
TITLE Loftus, B., Shetty, J., Severson, D., Brown, S. and Knudson, D.
JOURNAL End sequencing of Aedes aegypti BACs
COMMENT Unpublished (2003)
Other_GSSs: CSU-K33r.24N21.SP6

Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208

Email: enta@tigr.org
Library was provided by Susan Brown and Dennis Knudson at Colorado
State University.

Seq primer: T7

Class: BAC ends.

FEATURES

Location/Qualifiers
1. .938
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Rexville"
/db_xref="taxon:7159"
/clone="CSU-K33r.24N21"

/clone_lib="CSU-K33r"
/note="Vector: pBelosAC11; Site_1: HindIII"

ORIGIN

Query Match 87.0%; Score 17.4; DB 8; Length 938;
Best Local Similarity 94.7%; Pred. No. 8.9e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CTTGAAGGGATTCCCTC 19
|||||
Db 846 CTTGAAGGGATTCCCTC 864

Search completed: December 28, 2004, 10:09:04
Job time : 2996 secs

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